

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=1; day=27; hr=12; min=24; sec=3; ms=794;]

=====

Application No: 07110791 Version No: 1.0

Input Set:

Output Set:

Started: 2010-01-15 16:50:32.766
Finished: 2010-01-15 16:50:33.166
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 400 ms
Total Warnings: 0
Total Errors: 0
No. of SeqIDs Defined: 4
Actual SeqID Count: 4

SEQUENCE LISTING

<110> The United States of America, as represented by the
Secretary, Department of Health and Human Services
King, C. Richter
Kraus, Matthias H.
Aaronson, Stuart A.

<120> HUMAN GENE RELATED TO BUT DISTINCT FROM EGF RECEPTOR GENE

<130> 6137NCI-24

<140> 07110791

<141> 2010-01-15

<160> 4

<170> PatentIn version 3.5

<210> 1

<211> 78

<212> PRT

<213> Homo sapiens

<400> 1

Gly	Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala
1				5				10						15	

Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp
			20					25					30		

Phe	Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala
		35					40					45			

Asp	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu
	50					55					60				

Arg	Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly
65					70					75			

<210> 2

<211> 424

<212> DNA

<213> Homo sapiens

<400> 2

gtctacatgg	gtgcttccca	ttccagggga	tgagctacct	ggaggatgtg	cggctcgtac	60
------------	------------	------------	------------	------------	------------	----

acagggactt	ggccgctcgg	aacgtgctgg	tcaagagtcc	caaccatgtc	aaaattacag	120
------------	------------	------------	------------	------------	------------	-----

acttcgggct ggctcggctg ctggacattg acgagacaga gtaccatgca gatgggggca	180
aggttaggtg aaggaccaag gagcagagga ggctgggtgg agtggtgtct agcccatggg	240
agaactctga gtggccacct cccacaaca cacagttgga ggacttcctc ttctgccctc	300
ccaggtgccc atcaagtgga tggcgctgga gtccattctc cgccggcggt tcaccacca	360
gagtgatgtg tggagttatg gtgtgtgatg gggggtgttg ggaggggtgg gtgaggagcc	420
atgg	424

<210> 3
 <211> 5532
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)..(3816)

<400> 3	
gccgcgctgc gccggagtcc cgagctagcc ccggcgccgc cgccgcccag accggacgac	60
agggcacctc gtccggctcc gcccgagtcc ccgcctcgcc gccaacgcca caaccaccgc	120
gcacggcccc ctgactccgt ccagtattga tcgggagagc cggagcgagc tcttcgggga	180
gcagcg atg cga ccc tcc ggg acg gcc ggg gca gcg ctc ctg gcg ctg	228
Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu	
1 5 10	
ctg gct gcg ctc tgc ccg gcg agt cgg gct ctg gag gaa aag aaa gtt	276
Leu Ala Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val	
15 20 25 30	
tgc caa ggc acg agt aac aag ctc acg cag ttg ggc act ttt gaa gat	324
Cys Gln Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp	
35 40 45	
cat ttt ctc agc ctc cag agg atg ttc aat aac tgt gag gtg gtc ctt	372
His Phe Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu	
50 55 60	
ggg aat ttg gaa att acc tat gtg cag agg aat tat gat ctt tcc ttc	420
Gly Asn Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe	
65 70 75	
tta aag acc atc cag gag gtg gct ggt tat gtc ctc att gcc ctc aac	468
Leu Lys Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn	
80 85 90	
aca gtg gag cga att cct ttg gaa aac ctg cag atc atc aga gga aat	516
Thr Val Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn	
95 100 105 110	

atg tac tac gaa aat tcc tat gcc tta gca gtc tta tct aac tat gat	564
Met Tyr Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp	
115 120 125	
 gca aat aaa acc gga ctg aag gag ctg ccc atg aga aat tta cag gaa	612
Ala Asn Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu	
130 135 140	
 atc ctg cat ggc gcc gtg cgg ttc agc aac aac cct gcc ctg tgc aac	660
Ile Leu His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn	
145 150 155	
 gtg gag agc atc cag tgg cgg gac ata gtc agc agt gac ttt ctc agc	708
Val Glu Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser	
160 165 170	
 aac atg tcg atg gac ttc cag aac cac ctg ggc agc tgc caa aag tgt	756
Asn Met Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys	
175 180 185 190	
 gat cca agc tgt ccc aat ggg agc tgc tgg ggt gca gga gag gag aac	804
Asp Pro Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn	
195 200 205	
 tgc cag aaa ctg acc aaa atc atc tgt gcc cag cag tgc tcc ggg cgc	852
Cys Gln Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg	
210 215 220	
 tgc cgt ggc aag tcc ccc agt gac tgc tgc cac aac cag tgt gct gca	900
Cys Arg Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala	
225 230 235	
 ggc tgc aca ggc ccc cgg gag agc gac tgc ctg gtc tgc cgc aaa ttc	948
Gly Cys Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe	
240 245 250	
 cga gac gaa gcc acg tgc aag gac acc tgc ccc cca ctc atg ctc tac	996
Arg Asp Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr	
255 260 265 270	
 aac ccc acc acg tac cag atg gat gtg aac ccc gag ggc aaa tac agc	1044
Asn Pro Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser	
275 280 285	
 ttt ggt gcc acc tgc gtg aag aag tgt ccc cgt aat tat gtg gtg aca	1092
Phe Gly Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr	
290 295 300	
 gat cac ggc tcg tgc gtc cga gcc tgt ggg gcc gac agc tat gag atg	1140
Asp His Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met	
305 310 315	
 gag gaa gac ggc gtc cgc aag tgt aag aag tgc gaa ggg cct tgc cgc	1188
Glu Glu Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg	
320 325 330	

aaa	gtg	tgt	aac	gga	ata	ggt	att	ggt	gaa	ttt	aaa	gac	tca	ctc	tcc	1236
Lys	Val	Cys	Asn	Gly	Ile	Gly	Ile	Gly	Glu	Phe	Lys	Asp	Ser	Leu	Ser	
335					340					345					350	
ata	aat	gct	acg	aat	att	aaa	cac	ttc	aaa	aac	tgc	acc	tcc	atc	agt	1284
Ile	Asn	Ala	Thr	Asn	Ile	Lys	His	Phe	Lys	Asn	Cys	Thr	Ser	Ile	Ser	
				355					360					365		
ggc	gat	ctc	cac	atc	ctg	ccg	gtg	gca	ttt	agg	ggt	gac	tcc	ttc	aca	1332
Gly	Asp	Leu	His	Ile	Leu	Pro	Val	Ala	Phe	Arg	Gly	Asp	Ser	Phe	Thr	
			370					375					380			
cat	act	cct	cct	ctg	gat	cca	cag	gaa	ctg	gat	att	ctg	aaa	acc	gta	1380
His	Thr	Pro	Pro	Leu	Asp	Pro	Gln	Glu	Leu	Asp	Ile	Leu	Lys	Thr	Val	
		385					390					395				
aag	gaa	atc	aca	ggg	ttt	ttg	ctg	att	cag	gct	tgg	cct	gaa	aac	agg	1428
Lys	Glu	Ile	Thr	Gly	Phe	Leu	Leu	Ile	Gln	Ala	Trp	Pro	Glu	Asn	Arg	
	400					405					410					
acg	gac	ctc	cat	gcc	ttt	gag	aac	cta	gaa	atc	ata	cgc	ggc	agg	acc	1476
Thr	Asp	Leu	His	Ala	Phe	Glu	Asn	Leu	Glu	Ile	Ile	Arg	Gly	Arg	Thr	
415					420					425					430	
aag	caa	cat	ggt	cag	ttt	tct	ctt	gca	gtc	gtc	agc	ctg	aac	ata	aca	1524
Lys	Gln	His	Gly	Gln	Phe	Ser	Leu	Ala	Val	Val	Ser	Leu	Asn	Ile	Thr	
			435					440					445			
tcc	ttg	gga	tta	cgc	tcc	ctc	aag	gag	ata	agt	gat	gga	gat	gtg	ata	1572
Ser	Leu	Gly	Leu	Arg	Ser	Leu	Lys	Glu	Ile	Ser	Asp	Gly	Asp	Val	Ile	
		450						455					460			
att	tca	gga	aac	aaa	aat	ttg	tgc	tat	gca	aat	aca	ata	aac	tgg	aaa	1620
Ile	Ser	Gly	Asn	Lys	Asn	Leu	Cys	Tyr	Ala	Asn	Thr	Ile	Asn	Trp	Lys	
		465				470					475					
aaa	ctg	ttt	ggg	acc	tcc	ggt	cag	aaa	acc	aaa	att	ata	agc	aac	aga	1668
Lys	Leu	Phe	Gly	Thr	Ser	Gly	Gln	Lys	Thr	Lys	Ile	Ile	Ser	Asn	Arg	
	480					485					490					
ggt	gaa	aac	agc	tgc	aag	gcc	aca	ggc	cag	gtc	tgc	cat	gcc	ttg	tgc	1716
Gly	Glu	Asn	Ser	Cys	Lys	Ala	Thr	Gly	Gln	Val	Cys	His	Ala	Leu	Cys	
495					500					505					510	
tcc	ccc	gag	ggc	tgc	tgg	ggc	ccg	gag	ccc	agg	gac	tgc	gtc	tct	tgc	1764
Ser	Pro	Glu	Gly	Cys	Trp	Gly	Pro	Glu	Pro	Arg	Asp	Cys	Val	Ser	Cys	
			515						520					525		
cgg	aat	gtc	agc	cga	ggc	agg	gaa	tgc	gtg	gac	aag	tgc	aag	ctt	ctg	1812
Arg	Asn	Val	Ser	Arg	Gly	Arg	Glu	Cys	Val	Asp	Lys	Cys	Lys	Leu	Leu	
			530					535					540			
gag	ggt	gag	cca	agg	gag	ttt	gtg	gag	aac	tct	gag					

His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg	
560 565 570	
gga cca gac aac tgt atc cag tgt gcc cac tac att gac ggc ccc cac	1956
Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His	
575 580 585 590	
tgc gtc aag acc tgc ccg gca gga gtc atg gga gaa aac aac acc ctg	2004
Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu	
595 600 605	
gtc tgg aag tac gca gac gcc ggc cat gtg tgc cac ctg tgc cat cca	2052
Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro	
610 615 620	
aac tgc acc tac gga tgc act ggg cca ggt ctt gaa ggc tgt cca acg	2100
Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr	
625 630 635	
aat ggg cct aag atc ccg tcc atc gcc act ggg atg gtg ggg gcc ctc	2148
Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu	
640 645 650	
ctc ttg ctg ctg gtg gtg gcc ctg ggg atc ggc ctc ttc atg cga agg	2196
Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg	
655 660 665 670	
cgc cac atc gtt cgg aag cgc acg ctg cgg agg ctg ctg cag gag agg	2244
Arg His Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg	
675 680 685	
gag ctt gtg gag cct ctt aca ccc agt gga gaa gct ccc aac caa gct	2292
Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala	
690 695 700	
ctc ttg agg atc ttg aag gaa act gaa ttc aaa aag atc aaa gtg ctg	2340
Leu Leu Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu	
705 710 715	
ggc tcc ggt gcg ttc ggc acg gtg tat aag gga ctc tgg atc cca gaa	2388
Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu	
720 725 730	
ggt gag aaa gtt aaa att ccc gtc gct atc aag gaa tta aga gaa gca	2436
Gly Glu Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala	
735 740 745 750	
aca tct ccg aaa gcc aac aag gaa atc ctc gat gaa gcc tac gtg atg	2484
Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met	
755 760 765	
gcc agc gtg gac aac ccc cac gtg tgc cgc ctg ctg ggc atc tgc ctc	2532
Ala Ser Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu	
770 775 780	
acc tcc acc gtg caa ctc atc acg cag ctc atg ccc ttc ggc tgc ctc	2580
Thr Ser Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu	

785	790	795	
ctg gac tat gtc cgg gaa cac aaa gac aat att ggc tcc cag tac ctg			2628
Leu Asp Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu			
800	805	810	
ctc aac tgg tgt gtg cag atc gca aag ggc atg aac tac ttg gag gac			2676
Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp			
815	820	825	830
cgt cgc ttg gtg cac cgc gac ctg gca gcc agg aac gta ctg gtg aaa			2724
Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys			
	835	840	845
aca ccg cag cat gtc aag atc aca gat ttt ggg ctg gcc aaa ctg ctg			2772
Thr Pro Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu			
	850	855	860
ggt gcg gaa gag aaa gaa tac cat gca gaa gga ggc aaa gtg cct atc			2820
Gly Ala Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile			
	865	870	875
aag tgg atg gca ttg gaa tca att tta cac aga atc tat acc cac cag			2868
Lys Trp Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln			
	880	885	890
agt gat gtc tgg agc tac ggg gtg acc gtt tgg gag ttg atg acc ttt			2916
Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe			
895	900	905	910
gga tcc aag cca tat gac gga atc cct gcc agc gag atc tcc tcc atc			2964
Gly Ser Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile			
	915	920	925
ctg gag aaa gga gaa cgc ctc cct cag cca ccc ata tgt acc atc gat			3012
Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp			
	930	935	940
gtc tac atg atc atg gtc aag tgc tgg atg ata gac gca gat agt cgc			3060
Val Tyr Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg			
	945	950	955
cca aag ttc cgt gag ttg atc atc gaa ttc tcc aaa atg gcc cga gac			3108
Pro Lys Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp			
	960	965	970
ccc cag cgc tac ctt gtc att cag ggg gat gaa aga atg cat ttg cca			3156
Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro			
975	980	985	990
agt cct aca gac tcc aac ttc tac cgt gcc ctg atg gat gaa gaa gac			3204
Ser Pro Thr Asp Ser Asn Phe Tyr Arg Ala Leu Met Asp Glu Glu Asp			
	995	1000	1005
atg gac gac gtg gtg gat gcc gac gag tac ctc atc cca cag cag			3249
Met Asp Asp Val Val Asp Ala Asp Glu Tyr Leu Ile Pro Gln Gln			
	1010	1015	1020

ggc ttc ttc agc	agc ccc tcc acg tca	cgg act ccc ctc ctg	agc	3294
Gly Phe Phe Ser	Ser Pro Ser Thr Ser	Arg Thr Pro Leu Leu	Ser	
1025	1030	1035		
tct ctg agt gca	acc agc aac aat tcc	acc gtg gct tgc att	gat	3339
Ser Leu Ser Ala	Thr Ser Asn Asn Ser	Thr Val Ala Cys Ile	Asp	
1040	1045	1050		
aga aat ggg ctg	caa agc tgt ccc atc	aag gaa gac agc ttc	ttg	3384
Arg Asn Gly Leu	Gln Ser Cys Pro Ile	Lys Glu Asp Ser Phe	Leu	
1055	1060	1065		
cag cga tac agc	tca gac ccc aca ggc	gcc ttg act gag gac	agc	3429
Gln Arg Tyr Ser	Ser Asp Pro Thr Gly	Ala Leu Thr Glu Asp	Ser	
1070	1075	1080		